

RESULT 2
O9SEW4 PRELIMINARY: PRT: 593 AA.
AC O9SEW4: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid I;
OC Fagales; Juglandaceae; Juglans.
OX NCBI_TaxID=51240;
GN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAD; TISSUE=SONATIC EMBRYO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,
Jug r 2, from English walnut kernel (Juglans regia): a major food
allergen.";
RT Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF066055; AAF18269.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAW: PF00546; Seedstore_7s: 1.
FT NON_TER 1
SQ SEQUENCE 593 AA: 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 38.4%; Score 105.5; DB 10; Length 593;
Best Local Similarity 29.0%; Pred. No. 1.3e-05;
Matches 18; Conservative 13; Mismatches 12; Indels 19; Gaps 1;
OY 4 DDPKRYEDCRRRCCEMDTRGOKEQOQCEESCKSQY-----GKDDQOQ 44
DB 118 DDQOYHRCQRCQIOEOSPERRQCQRCERQYKQGRGPEASPRRESRGREEO 177
OY 45 RH 46
DB 178 RH 179

RESULT 3
O9SPL4 PRELIMINARY: PRT: 666 AA.
AC O9SPL4: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161884; AAD54245.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAW: PF00546; Seedstore_7s: 1.
SQ SEQUENCE 666 AA: 78243 MW; 0ECA22F8710F8A7B CRC64;

Query Match 34.2%; Score 94; DB 10; Length 666;
Best Local Similarity 35.6%; Pred. No. 0.00042;

Matches 16; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
OY 3 DDPKRYEDCRRRCCEMDTRGOKEQOQCEESCKSQYGEKDQOORH 47
DB 76 DDPQTCCQCCQRCRCROESGPRQOYCORCKEICEEBEERYNR 120

RESULT 4
O9SPL5 PRELIMINARY: PRT: 666 AA.
AC O9SPL5: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161883; AAD54244.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAW: PF00546; Seedstore_7s: 1.
SQ SEQUENCE 666 AA: 78217 MW; C752B884B2DF0224 CRC64;

Query Match 33.5%; Score 92; DB 10; Length 666;
Best Local Similarity 33.3%; Pred. No. 0.00075;
Matches 15; Conservative 9; Mismatches 21; Indels 0; Gaps 0;
OY 3 DDPKRYEDCRRRCCEMDTRGOKEQOQCEESCKSQYGEKDQOORH 47
DB 76 EDPQTCCQCCQRCRCROESGPRQOYCORCKEICEEBEERYNR 120

RESULT 5
O9ZW13 PRELIMINARY: PRT: 810 AA.
AC O9ZW13: 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PV100.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid I;
OC Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KURUKAWA AMAKURI NANKIN; TISSUE=COTYLEDON;
RX MEDLINE=99107919; PubMed=9891029;
RA Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura I.;
RT "Multiple functional proteins are produced by cleaving Asn-Gln bonds
RT of a single precursor by vacuolar processing enzyme.";
RL J. Biol. Chem. 274:2563-2570(1999).
DR EMBL: AB019195; BAA34056.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFAW: PF00546; Seedstore_7s: 1.
DR PRODOM: PD081059; -; 1.
SQ SEQUENCE 810 AA: 97314 MW; A829A3F7542266AB CRC64;

Query Match 32.7%; Score 90; DB 10; Length 810;

Best Local Similarity 39.5%; Pred. No. 0.0016;
Matches 15; Conservative 10; Mismatches 13; Indels 0; Gaps 0.

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Oy 5 PKRYEDCRRRCWDTRGQKEOQQCEESCKSQYGEKD 42
    | | | | | : | : : | : | : | : |
Db 74 PRAIEYECRLRCQVAREGVEODORKCEOVCEERLREEO 111

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RESULT	6	
ID	Q9SPL3	PRELIMINARY;
	Q9SPL3	PRT; 625 AA.

DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).

OS *Macadamia integrifolia* (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxId=60698;

RP SEQUENCE FROM N.A.
RC TISSUE=NOT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Mannens J.M.;
TT "A family of antimicrobial peptides is produced by processing of a 7S

plant J. 0:0:0(1999).
 RL
 EMBL: AF161885; AAD54246.1; -.
 DR
 HSSP: P02853; 2PBL.
 DR
 INTERPRO: IPR001113; -.

BA *ferny, f100340, secuscore_1s, 1.*
 FT NON_TER 1 1
 SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query match	32.0%	Score 88	DB 10	Length 625
Best Local Similarity	29.5%	Pred. No. 0.0023		
Matches	13	Conservative	15	Mismatches 16; Indels 0; Gaps 0

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Db      80 DPQQVEGQCKRCORRETEPRNMGICQRCERCERYEKEKRQKQR 123

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Q9ZTP0		
ID	Q9ZTP0	PRELIMINARY; PRT; 393 AA.
AC	Q9ZTP0;	
DT	01-MAY-1999 (TREMBLrel. 10, Created)	
01-MAY-1999 (TREMBLrel. 10, Created)		

DT 01-MAY-1999 (TREMBLrel. 10, last annotation update)
DE HYPOTHETICAL 45.3 KDA PROTEIN.
GN OSE705.
OS *Oryza sativa* (Rice).
ID 1

OC Magnoliophyta: Liliopsida; Poales; Poaceae; Oryza.
OX NCBJ_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.

RA Chen P.W., Chen L.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF049348; AF002494.1; -
 KW Hypothetical protein.

Query match	30.08;	Score 82.5;	DB 10;	Length 393;
Best local Similarity	28.6%;	Pred. No. 0.0074;		

QY 1 GDDDPKRYEDCRRCEWDT-RGQKEQQCEESC--KSQYGEKDDQQRH 46

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Db      | || : ||::| | : ||::| | : | : | : |
32 GRDPKEELRWCKOCRWEAGODOROLRECEEQCLOROEDDDDDENTH 80
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RESULT	8
Q9V7P3	
ID	Q9V7P3
PRELIMINARY:	
PRT:	541 AA

AC	Q9VFE3	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)
DE	C65262	PROTEIN

GN *C96d6.2.*
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Eurytomidae; Drosophilidae; Drosophilinae

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OX NCBI_TaxID=1227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
C  MERRILL-2010C007  D-14-2 10221130

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RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Goocayne J.D.,
RA Manalilides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Woltman J.R., Vandell M.D., Zhang Q., Chen L.X.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayan A., An H.-J., Andrews-Plinnhoff C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu I., Neasey E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu F., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahile C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,

R.A. Kozlovskiy, V.P. Mazurenko, E.F. Naiplov, G.M. Oshin,
R.A. Orlovskiy, R.I. Pashchenko, A.V. Reznichenko, N.S.
RA Kimmel B.E., Kodira C.D., Kiriloff C., Kravtsev S., Kulp D., Lal Z.,
RA Laško P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosneger A.,
RA Merkulyov G., Mishina N.V., Mobarry C., Morris J., Mosneger A.

RA Nelson D.R., Moly M., Mulvey E., Mulvey D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shire B.C., Sildenafil K., Simmons M., Skunkin M.P., Smith P.,
RA Shire B.C., Sildenafil K., Simmons M., Skunkin M.P., Smith P.,

RA Spher E, Spalding A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye T., Yeh R.-F., Zaveri I. S., Zhan M., Zhang G., Zhao Q., Zhou F.

KA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,"
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
PMID: AF003607, AF559004 1, 2

DR FLYBASE: FBgn034121; CG6262.
SQ SEQUENCE 541 AA; 58080 MW; 83BEA5FE510F7C8F CRC64;

0Y 2 DDDPPKRYEDCRRRCMDTR--GCKEQQQCEKSCSKSYQYGEKQDQQRHR 47
Best Local Similarity 39.6%; Pred. No. 0.8;
Matches 19; Conservative 5; Mismatches 13; Indels 11; Gaps 4

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Db      234 DTF-----DC--ECSMDERQKQMEQKQKQDDCMRQ--Q000000EHQ 272

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RESULT 9
P1419 PRELIMINARY: PRT: 411 AA.
AC P91419:
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CODD FOR BY C. ELEGANS CDNA YK15A6.5.
GN T01D1.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Wellstock L., Wilkinson-Sproat J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Bradshaw H., Woldmann P.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U80455; AAB37887.1; -;
SQ SEQUENCE 411 AA: 44675 MW: 599DAC9DCFA1382 CRC64;

Query Match 23.8%; Score 65.5; DB 5; Length 411;
Best Local Similarity 35.9%; Pred. No. 1.1;
Matches 14; Conservative 11; Mismatches 11; Indels 3; Gaps 2;

OY 10 EDCRRRCWMDTRGQK-000CEESCKS--OYGEKDOQR 45
DB 147 OPCOACPPQOQPOOQOCCOTCQSDPDQYSQOLIQQ 185

RESULT 10
O9VPS3 PRELIMINARY: PRT: 554 AA.
AC O9VPS3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG2839 PROTEIN (FRAGMENT).
GN CG2839.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Meruliov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relneert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Wellstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AB003588; AAF51469.1; -;
DR FLYBASE: FBgn0031273; CG2839.
DR INTERPRO: IPR001304; -;
DR PFAM: PF00059; Ictin_G_1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
FT NON_TER 554 554
SQ SEQUENCE 554 AA: 69873 MW: 029B6D852609FD16 CRC64;

Query Match 23.6%; Score 65; DB 5; Length 554;
Best Local Similarity 35.9%; Pred. No. 1.7;
Matches 14; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

OY 7 KRYEDCRRCWMDTRGQKFOQCEESCKSOYGEKDOQR 45
DB 468 RRREKRREERREERREERREERREERREERREERREER 506

RESULT 11
O9P2D9 PRELIMINARY: PRT: 1298 AA.
AC O9P2D9:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE KIA1408 PROTEIN (FRAGMENT).
GN KIA1408.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX Nagase T., Kikuno R., Ishikawa K., Hirokawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.

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